

1/19

5' GTG CCC ATG CTG GGC AAC CCC CTG <sup>10</sup> <sup>19</sup> <sup>28</sup> <sup>37</sup> <sup>46</sup> <sup>55</sup>  
-----  
Val Cys His Val Ile Phe Lys Asn Gln Arg

ATG CAC TCG GCC ACC ACC CTC TTC ATC GTC AAC CTG GCA GTT CCC GAC ATA ATG  
<sup>64</sup> <sup>73</sup> <sup>82</sup> <sup>91</sup> <sup>100</sup> <sup>109</sup>  
Met His Ser Ala Thr Ser Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met

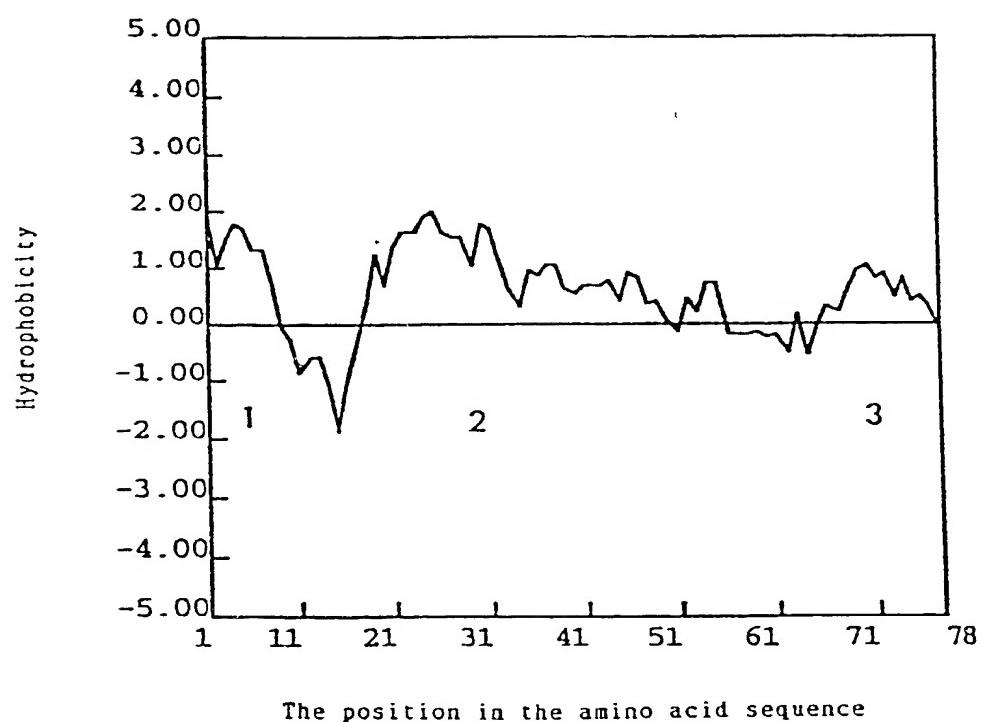
ATC ACG CTG CTC AAC ACC CCC TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG  
<sup>118</sup> <sup>127</sup> <sup>136</sup> <sup>145</sup> <sup>154</sup> <sup>163</sup>  
Ile Thr Leu Leu Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp

ATA TTT GGG AAG GGC ATG TCC CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG  
<sup>172</sup> <sup>181</sup> <sup>190</sup> <sup>199</sup> <sup>208</sup> <sup>217</sup>  
Ile Phe Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu

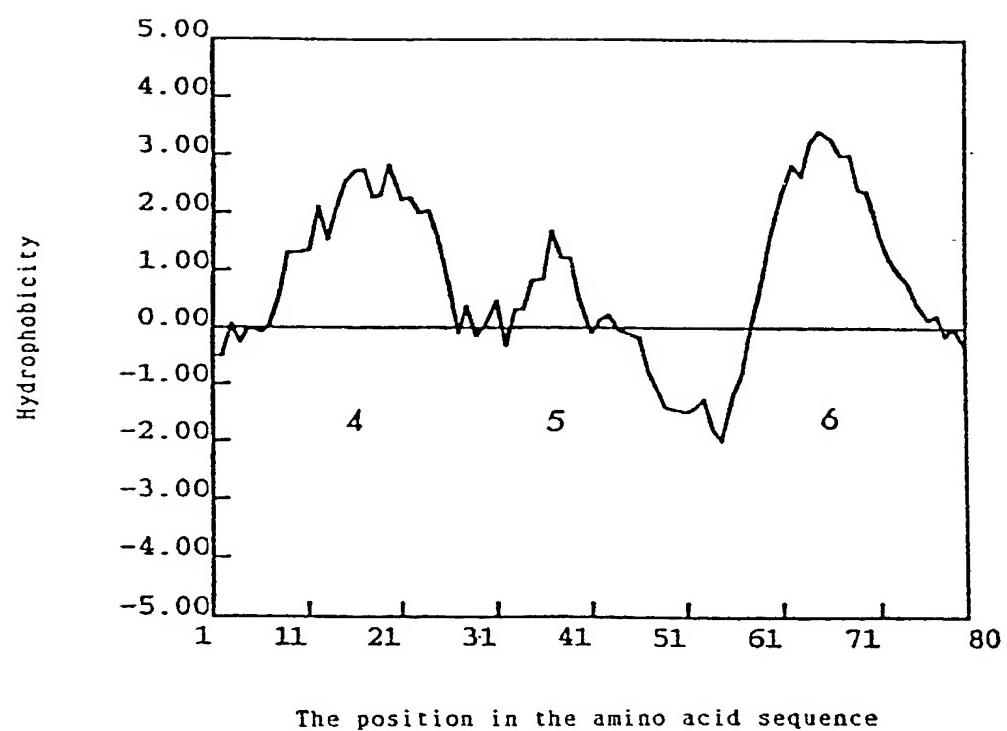
CAC GTC TCA GCA CTG ACA 3'  
<sup>226</sup> <sup>235</sup>  
His Val Ser Ala Leu Thr

5' 9 18 27 36 45 54  
GAG CCC GCT GAC CTC TTC TGG AAG AAC CTG GAC TTG CCC ACC TTC ATC CTG CTC  
-----  
Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile Leu Leu  
  
63 72 81 90 99 108  
AAC ATC CTG CCC CTC CTC ATC ATC TCT GTG GCC TAC GTT CGT GTG ACC ACC AAG AAA  
-----  
Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg Val Thr Lys Lys  
  
117 126 135 144 153 162  
CTG TGG CTG TGT AAT ATG ATT GTC GAT GTG ACC ACA GAG CAG TAC TTT GGC CTG  
-----  
Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu  
  
171 180 189 198 207 216  
CGG CCC AAA AAG AAG AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT  
-----  
Arg Pro Lys Lys Lys Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe  
  
225 234  
GCC CTC TGC TGG TTG CCT CTC GAC 3'  
-----  
Ala Leu Cys Trp Leu Pro Leu Asp

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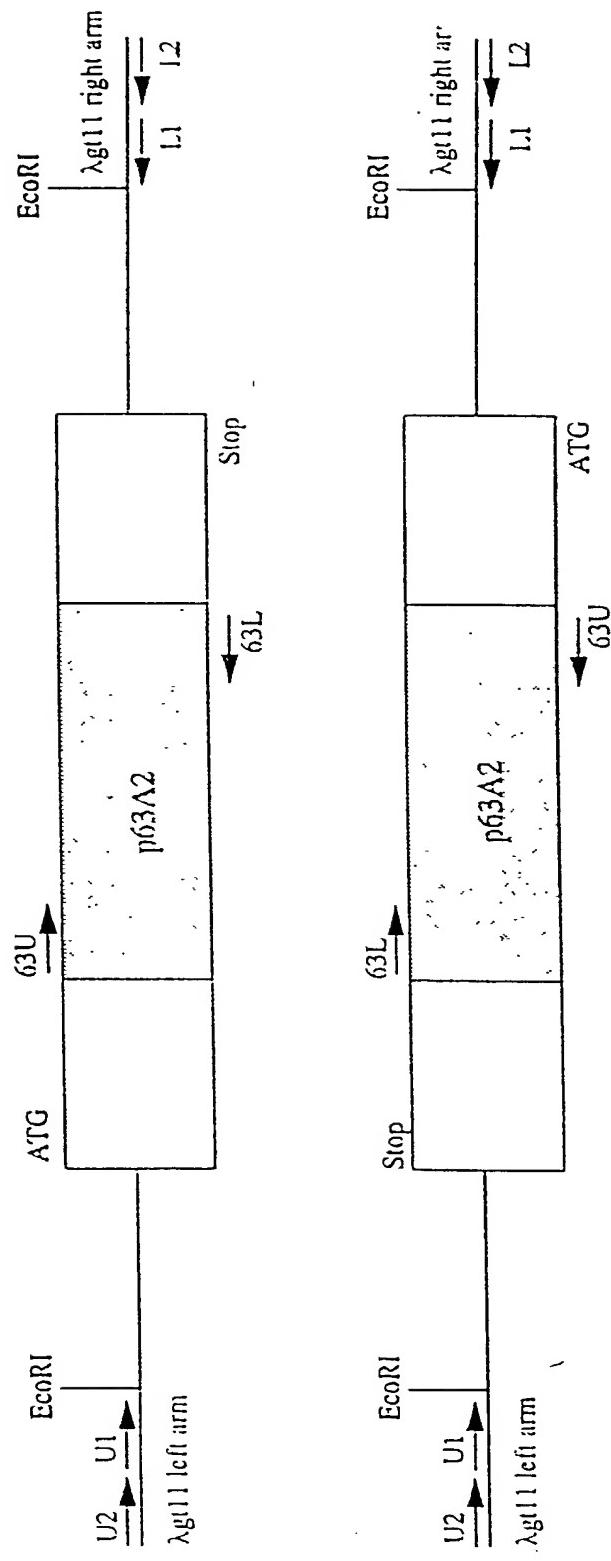
4/19



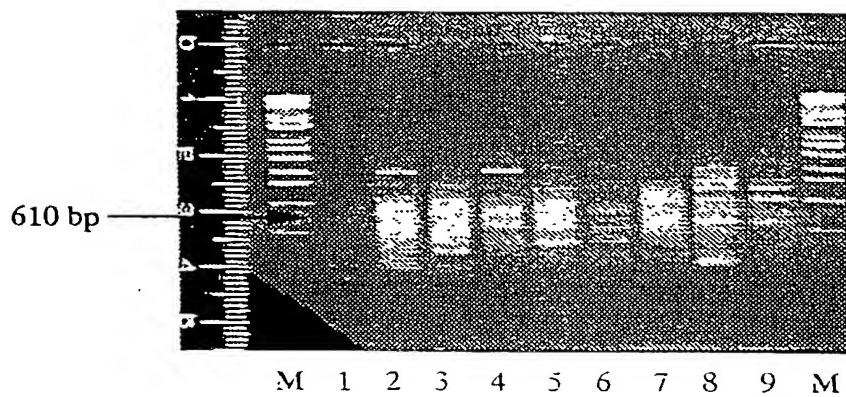
5/19

p63A2 P30731	10 1	VCHVIFKQRF VCHVIFKQRF	MHSATSLFIV MHSATSLFIV	NIAVADIMIT NIAVADIMIT	LLNTPFTLVR LLNTPFTLVR	EVNSTWIFGK EVNSTWIFGK	50 50.
p63A2 P30731	60 51	GMCHVSRFQ GMCHVSRFQ	YCSLHVSALT YCSLHVSALT	LTAIAVDRHQ VIMHPLKPRI	SITKGVIYLA SITKGVIYLA		100 100
p63A2 P30731	110 101			120 130	140 EP	ADLEWKNLDL ADLEWKNLDL	150 150
p63A2 P30731	160 151	PTFILNLIP ATFILYLIP	LLTISYAYRN LFTISYAYRN	VTKGWLCLNM YAKKLWLCNT	IVDVTTEQYF IGDVTTEQYL	ALRPKKAKTI ALRRKGKTTV	200 200
p63A2 P30731	210 201	KHLMLVVVF EMLVLVVVF	.....	220 230	240 .....	250 .....	250 250

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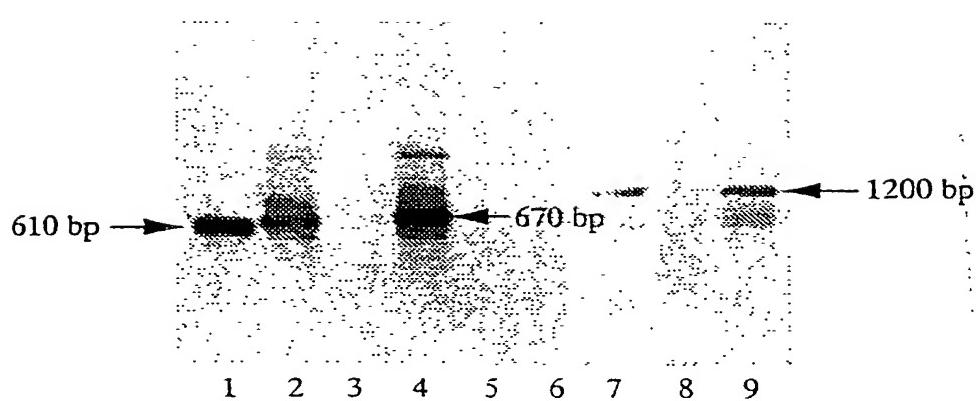
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M :  $\lambda$  DNA / Sty I marker

- lane 1 ; 63U~63L
- lane 2 ; U1~63U
- lane 3 ; U1~63L
- lane 4 ; U2~63U
- lane 5 ; U2~63L
- lane 6 ; L1~63U
- lane 7 ; L1~63L
- lane 8 ; L2~63U
- lane 9 ; L2~63L

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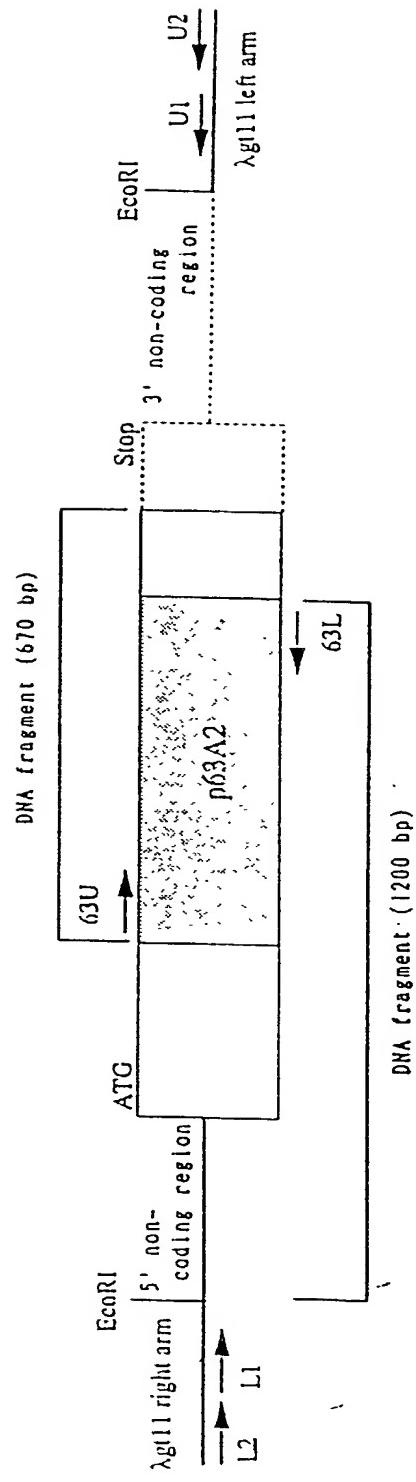
- lane 1 ; 63U~63L
- lane 2 ; U1~63U
- lane 3 ; U1~63L
- lane 4 ; U2~63U
- lane 5 ; U2~63L
- lane 6 ; L1~63U
- lane 7 ; L1~63L
- lane 8 ; L2~63U
- lane 9 ; L2~63L

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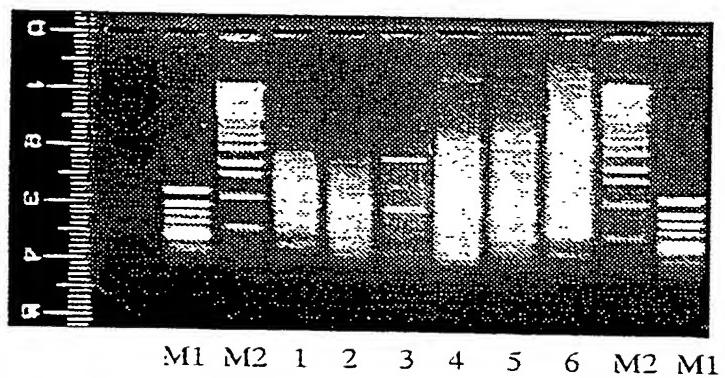
10/19

	10	20	30	40	50	60
OR16-F. SEQ	TTGCCCTCCYCATCATCTCTGTGGCCTACGCYCGTGTGGCCAARAAACTGTGGCTGTGT					
MUSGIR. DNA	CTTCCACTCTTCATTATCTCAGTGGCTATGCTCGTGTGGCCAAGAACGCTGTGGCTCTGT					
	1030	1040	1050	1060	1070	1080
		70	80	90	100	110
OR16-F. SEQ	AATATGATTGGCGATGTGACCACAGAGCAGTACCTTG-CCTKCGGCGCAAAAAGAAGAAG					
MUSGIR. DNA	AAACACCATTGGCGACGTGACCACAGAGCAGTACCTCGCCCTGCGACGCAAGAAGAACCC					
	1090	1100	1110	1120	1130	1140
	120	130	140	150	160	170
OR16-F. SEQ	ACCATCAAGATGTTGATGCTGGTAGTCCCCCTTGCCCTCCGCTGGTTCCCCCTCAAC					
MUSGIR. DNA	ACCGTGAAGATGCTGGTAGTCCCTCTTGCCCTCTGCTGGTTCCCTCAAC					
	1150	1160	1170	1180	1190	1200
	180	190	200	210		
OR16-F. SEQ	TGCTACGTCCCTCCTGTCCAGCAAGGTCAATCCGC					
MUSGIR. DNA	TGCTATGTCCTCTTGTCCAGCAAGGCCATCCAC					
	1210	1220	1230	1240		

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M1 ;  $\phi$ X174 / HincII

M2 ;  $\lambda$  / StyI

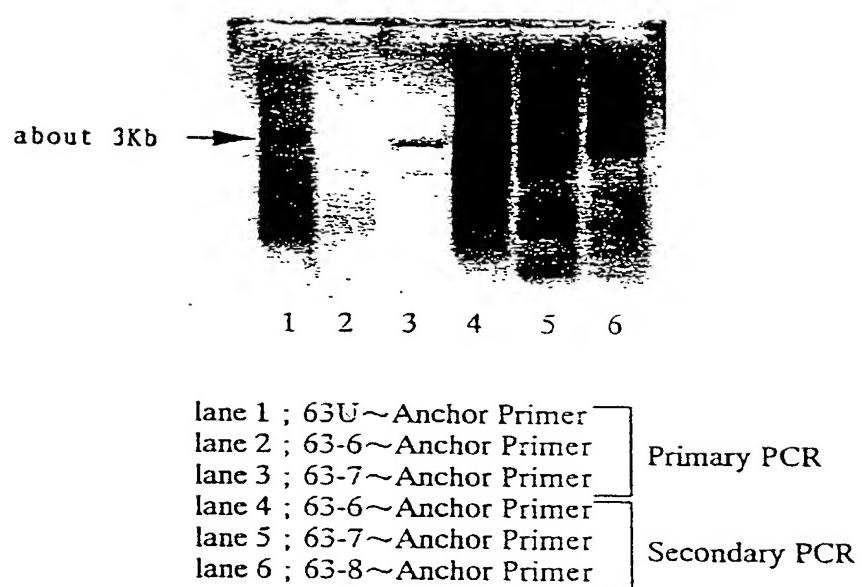
lane 1 ; 63U~Anchor Primer  
lane 2 ; 63-6~Anchor Primer  
lane 3 ; 63-7~Anchor Primer  
lane 4 ; 63-6~Anchor Primer  
lane 5 ; 63-7~Anchor Primer  
lane 6 ; 63-8~Anchor Primer

Primary PCR

Secondary PCR

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

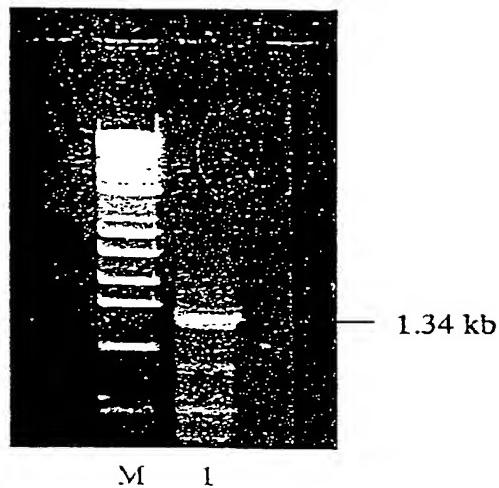
13/19



14/19

	10	20	30	40	50	60
63A2-3' . seq	CCCTCTGCTGGTCCCCCTCAACTGCTACGTCCCTCCTGTCCAGCAAGGTATCCGCA					
MUSGIR. DNA	X::::::::::: ::::::::::: ::::::::::: ::::::::::: ::::::: :::					
	CCCTCTGCTGGTCCCCCTCAACTGCTATGTCCCTCCTGTCCAGCAAGGCCATCCACA					
	1190 1200 1210 1220 1230 1240					
	70	80	90	100	110	120
63A2-3' . seq	CCAACAATGCCCTCTACTTTGCCTTCACTGGTTGCCATGAGCAGCACCTGCTATAACC					
MUSGIR. DNA	::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::					
	CCAACAATGCCCTCTACTTTGCCTTCACTGGTTGCCATGAGCAGTACTGTTATAACC					
	1250 1260 1270 1280 1290 1300					
	130	140	150	160	170	180
63A2-3' . seq	CCTTCATATACTGCTGGCTAACGAGAACTTCAGGATTGAGCTAAAGGCATTACTGAGCA					
MUSGIR. DNA	::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::					
	CCTTCATCTACTGCTGGCTCAATGAGAACTTAGGGTTGAGCTTAAGGCATTGCTGAGCA					
	1310 1320 1330 1340 1350 1360					
	190	200	210	220	230	240
63A2-3' . seq	TGTGTCAAAAGACCTCCAAAGCCTCAGGAGGACAGGCCACCCCTCCCCAGTTCCTTCCTCA					
MUSGIR. DNA	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::					
	TGTGCAAAAGGCCACCCAAAGCGCAGGAAGACAGGCTACCCCTCCCCAGTTCTTCCTCA					
	1370 1380 1390 1400 1410 1420					
	250	260	270	280	290	300
63A2-3' . seq	GGGTGGCCTGGACAGAGAAGATGATGCCAGAGGGCTCCCCCTGCCATAACCTCTGC					
MUSGIR. DNA	::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::::::: ::					
	GGGTGGCATGGACAGAGAAGGCCATGGTCGGAGGGCTCCACTACCTAATCACCACTTGC					
	1430 1440 1450 1460 1470 1480					
	310	320	330	340	350	360
63A2-3' . seq	CCACCTCCCAACTCCAGTCTGGGAAGACAGACCTGTATCTGTGGAACCCATTGTGACGA					
MUSGIR. DNA	:: : ::::: ::::::::::::::: ::::::::::::::: ::::::::::::::: :: :					
	CCTCTCCCAGATCCAGTCTGGGAAGACAGATCTGTATCTGTGGAACCCGTTGTGCCA					
	1490 1500 1510 1520 1530 1540					
	370	380	390	400	410	
63A2-3' . seq	TGAGT <u>TA</u> AGAGGTTGGGAAGAGGGAGTGGGAGGGTCTGT-CTC-CAC-CTGAGGCAG					
MUSGIR. DNA	::::::: :: : ::::::: :: : ::::::: :: : ::::: :: : :: :					
mouse CIR stop codon	TGAGT <u>TA</u> GGAAAGCT-GGAAGTTGGTGGGGAGGGTCTTCCTCTCACATTGACCAAG					
	1550 1560 1570 1580 1590 1600					
	420	430	440	450	460	470
63A2-3' . seq	GGA--AAGAGAG-CCTATTCTCACACATGATC-TTCAGAGTGCTGGAAACACACTCTGC					
MUSGIR. DNA	::ACACTAACAGAGTTGGAAAGTAACACAGAAGCAGTGAGA-TGCTTGGGTTCTAGGAACC					
	1610 1620 1630 1640 1650 1660					
	480	490				
63A2-3' . seq	AGAAGCTGTAGGACTCTTGAAT					
MUSGIR. DNA	TGTCCAGCCCCATCTGATTGCA					
	1670 1680					

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M ;  $\lambda$  / StyI  
lane 1 ; Whole Brain

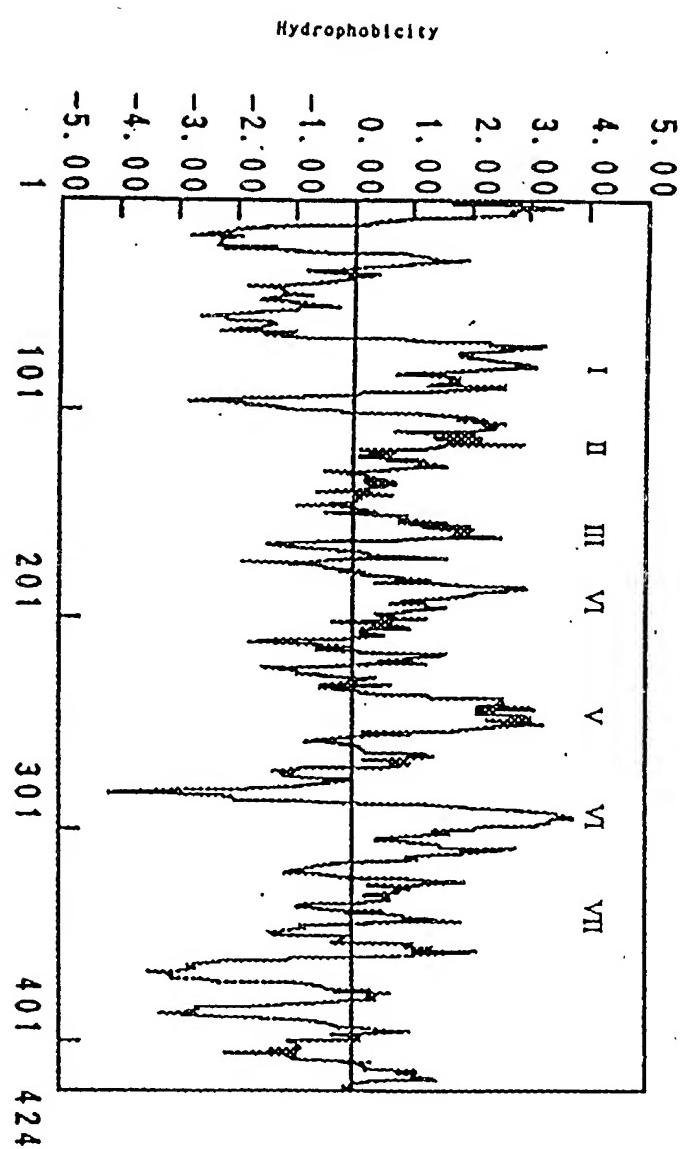
## 16/19

9            18            27            36            45            54  
 S' ATG GTC CCT CAC CTC TTG CTG CTC TGT CTC CTC CCC TTG GTG CGA GCC ACC GAG  
 --- --- --- --- --- ---  
 Met Val Pro His Leu Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala Thr Glu  
  
 63            72            81            90            99            108  
 CCC CAC GAG GGC CGG GCC GAC GAG CAG AGC GCG GAG GCG GCC CTG GCC GTG CCC  
 --- --- --- --- --- ---  
 Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala Leu Ala Val Pro  
  
 117            126            135            144            153            162  
 AAT GCC TCG CAC TTC TTC TCT TGG AAC AAC TAC ACC TTC TCC GAC TGG CAG AAC  
 --- --- --- --- --- ---  
 Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr Phe Ser Asp Trp Gln Asn  
  
 171            180            189            198            207            216  
 TTT GTG GGC AGG AGG CGC TAC GGC GCT GAG TCC CAG AAC CCC ACG GTG AAA GCC  
 --- --- --- --- --- ---  
 Phe Val Gly Arg Arg Tyr Gly Ala Glu Ser Gln Asn Pro Thr Val Lys Ala  
  
 225            234            243            252            261            270  
 CTG CTC ATT GTG GCT TAC TCC TTC ATC ATT GTC TTC TCA CTC TTT GGC AAC GTC  
 --- --- --- --- --- ---  
 Leu Leu Ile Val Ala Tyr Ser Phe Ile Ile Val Phe Ser Leu Phe Gly Asn Val  
  
 279            288            297            306            315            324  
 CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA ATG CAC TCG GCC ACC AGC CTC  
 --- --- --- --- --- ---  
 Leu Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu  
  
 333            342            351            360            369            378  
 TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG ATC ACG CTG CTC AAC ACC CCC  
 --- --- --- --- --- ---  
 Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro  
  
 387            396            405            414            423            432  
 TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG ATA TTT GGG AAG GGC ATG TGC  
 --- --- --- --- --- ---  
 Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys  
  
 441            450            459            468            477            486  
 CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG CAC GTC TCA GCA CTG ACA CTG  
 --- --- --- --- --- ---  
 His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu Thr Leu  
  
 495            504            513            522            531            540  
 ACA GCC ATT GCG GTG GAT CGC CAC CAG GTC ATC ATG CAC CCC TTG AAA CCC CGG  
 --- --- --- --- --- ---  
 Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro Leu Lys Pro Arg  
  
 549            558            567            576            585            594  
 ATC TCA ATC ACA AAG GGT GTC ATC TAC ATC GCT GTC ATC TGG ACC ATG GCT ACG  
 --- --- --- --- --- ---  
 Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val Ile Trp Thr Met Ala Thr  
  
 603            612            621            630            639            648  
 TTC TTT TCA CTC CCA CAT GCT ATC TGC CAG AAA TTA TTT ACC TTC AAA TAC AGT  
 --- --- --- --- --- ---  
 Phe Phe Ser Leu Pro His Ala Ile Cys Gln Lys Leu Phe Thr Phe Lys Tyr Ser  
  
 657            666            675            684            693            702  
 GAG GAC ATT GTG CGC TCC CTC TGC CTG CCA GAC TTC CCT GAG CCA GCT GAC CTC  
 --- --- --- --- --- ---  
 Glu Asp Ile Val Arg Ser Leu Cys Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu

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711	720	729	738	747	756
TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC					
---	---	---	---	---	---
Phe Trp Lys Tyr Leu Asp Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu					
765	774	783	792	801	810
CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT					
---	---	---	---	---	---
Leu Ile Ile Ser Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn					
819	828	837	846	855	864
ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG CGG CGC AAA AAG AAG					
---	---	---	---	---	---
Met Ile Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys					
873	882	891	900	909	918
AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC					
---	---	---	---	---	---
Lys Thr Ile Lys Met Leu Met Val Val Val Leu Phe Ala Leu Cys Trp Phe					
927	936	945	954	963	972
CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT					
---	---	---	---	---	---
Pro Leu Asn Cys Tyr Val Leu Leu Ser Ser Lys Val Ile Arg Thr Asn Asn					
981	990	999	1008	1017	1026
GCC CTC TAC TTT GCC TTC CAC TGG TTT GCC ATG AGC AGC ACC TGC TAT AAC CCC					
---	---	---	---	---	---
Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro					
1035	1044	1053	1062	1071	1080
TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG					
---	---	---	---	---	---
Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe Arg Ile Glu Leu Lys Ala Leu Leu					
1089	1098	1107	1116	1125	1134
AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT					
---	---	---	---	---	---
Ser Met Cys Gln Arg Pro Pro Lys Pro Gln Glu Asp Arg Pro Pro Ser Pro Val					
1143	1152	1161	1170	1179	1188
CCT TCC TTC AGG GTG GCC TGG ACA GAG AAG AAT GAT GGC CAG AGG GCT CCC CTT					
---	---	---	---	---	---
Pro Ser Phe Arg Val Ala Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu					
1197	1206	1215	1224	1233	1242
GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA					
---	---	---	---	---	---
Ala Asn Asn Leu Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser					
1251	1260	1269			
TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3'					
---	---	---	---	---	---
Ser Val Glu Pro Ile Val Thr Met Ser ***					

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63A2. AMI MUSGIR. AMI	10 9KVPPLLE 9KVPPLLE	20 LIPV RATE LIPV RATE	30 HEGRAD EGS HEGRAD EGS	40 EANLVN EANLVN	50 HFFSINVF HFFSINVF	50 SHFWNYTF SHFWNYTF
63A2. AMI MUSGIR. AMI	60 51 SDWONFUGRA 51 SDWONFUGRA	70 RVAESONPT RVAESONPT	80 VKALLIVAVS VKALLIVAVS	90 FLVSEFGN FLVSEFGN	100 VLVCHWIFKN VLVCHWIFKN	100 100 100
63A2. AMI MUSGIR. AMI	110 101 QRMHSATSLF 101 QRMHSATSLF	120 VNLAVADIM VNLAVADIM	130 ITLNTPFTI ITLNTPFTI	140 VRFVJSTWIE VRFVJSTWIE	150 GKGMCHVSARF GKGMCHVSARF	150 150 150
63A2. AMI MUSGIR. AMI	160 151 AOVCSLHVSA 151 AOVCSLHVSA	170 LT AJAVDR LT AJAVDR	180 HOVIMHPLKP HOVIMHPLKP	190 RISTKGVY RISTKGVY	200 IAVIIWATF IAVIIWATF	200 200 200
63A2. AMI MUSGIR. AMI	210 201 FSLP HAI COK 201 FSLP HAI COK	220 LTFPKYSED LTFPKYSED	230 VRSCLCPDFP VRSCLCPDFP	240 EPADLFWKYL EPADLFWKYL	250 OLATFILLY OLATFILLY	250 250 250
63A2. AMI MUSGIR. AMI	260 251 LPLTISVAY 251 LPLTISVAY	270 ARVAKKLWL ARVAKKLWL	280 WIGDVTED WIGDVTED	290 WELRKKK WELRKKK	300 TKMLVWV TKMLVWV	300 300
63A2. AMI MUSGIR. AMI	310 301 LFALCWFLN 301 LFALCWFLN	320 CIVILLSSKY CIVILLSSKY	330 FNNNALYFA FNNNALYFA	340 FHWFAMSSTC FHWFAMSSTC	350 VHFIVCWL VHFIVCWL	350 350 350
63A2. AMI MUSGIR. AMI	360 351 ENFREELKAL 351 ENFREELKAL	370 LSMCORPPK LSMCORPPK	380 QDPRPSV QDPRPSV	390 SF RVANTEK SF RVANTEK	400 OEGEARLGN OEGEARLGN	400 400 400
63A2. AMI MUSGIR. AMI	410 401 LURPSQDSG 401 LURPSQDSG	420 <DLSSVEP <DLSSVEP	430 TMS..... TMS.....	440 ..... .....	450 ..... .....	450 450 450